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RAW SEQUENCE LISTING

DATE: 01/23/2002

PATENT APPLICATION: US/09/893,371

TIME: 19:13:40

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3 <110> APPLICANT: de Lanerolle, Primal
4     Nowak, Grzegorz
5     Pestic-Dragovich, Lidiya
6     Stojiljkovic, Ljuba
7     Hozak, Pavel
9 <120> TITLE OF INVENTION: Nuclear Myosin I B with A 16 Amino Acid N-Terminal
10    Extension
12 <130> FILE REFERENCE: 30151/92399
14 <140> CURRENT APPLICATION NUMBER: 09/893,371
15 <141> CURRENT FILING DATE: 2001-06-27
17 <150> PRIOR APPLICATION NUMBER: 60/214,944
18 <151> PRIOR FILING DATE: 2000-06-29
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1044
26 <212> TYPE: PRT
27 <213> ORGANISM: Artificial Sequence
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40 Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile Glu Asn Leu
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43 Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile Gly Pro Val
44     50             55             60
46 Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr Ser Arg Gln
47     65             70             75             80
49 His Met Glu Arg Tyr Arg Gly Val Ser Phe Tyr Glu Val Pro Pro His
50     85             90             95
52 Leu Phe Ala Val Ala Asp Thr Val Tyr Arg Ala Leu Arg Thr Glu Arg
53     100            105            110
55 Arg Asp Gln Ala Val Met Ile Ser Gly Glu Ser Gly Ala Gly Lys Thr
56     115            120            125
58 Glu Ala Thr Lys Arg Leu Leu Gln Phe Tyr Ala Glu Thr Cys Pro Ala
59     130            135            140
61 Pro Glu Arg Gly Gly Ala Val Arg Asp Arg Leu Leu Gln Ser Asn Pro
62     145            150            155            160
64 Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Leu Arg Asn Asp Asn Ser

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67 Ser Arg Phe Gly Lys Tyr Met Asp Val Gln Phe Asp Phe Lys Gly Ala
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70 Pro Val Gly Gly His Ile Leu Ser Tyr Leu Leu Glu Lys Ser Arg Val
71          195          200          205
73 Val His Gln Asn His Gly Glu Arg Asn Phe His Val Phe Tyr Gln Leu
74          210          215          220
76 Leu Glu Gly Gly Glu Glu Thr Leu Arg Arg Leu Gly Leu Glu Arg
77 225          230          235          240
79 Asn Pro Gln Ser Tyr Leu Tyr Leu Val Lys Gly Gln Cys Ala Lys Val
80          245          250          255
82 Ser Ser Ile Asn Asp Lys Ser Asp Trp Lys Val Met Arg Lys Ala Leu
83          260          265          270
85 Ser Val Ile Asp Phe Thr Glu Asp Glu Val Glu Asp Leu Leu Ser Ile
86          275          280          285
88 Val Ala Ser Val Leu His Leu Gly Asn Ile His Phe Ala Ala Asp Glu
89          290          295          300
91 Asp Ser Asn Ala Gln Val Thr Thr Glu Asn Gln Leu Lys Tyr Leu Thr
92 305          310          315          320
94 Arg Leu Leu Gly Val Glu Gly Thr Thr Leu Arg Glu Ala Leu Thr His
95          325          330          335
97 Arg Lys Ile Ile Ala Lys Gly Glu Glu Leu Leu Ser Pro Leu Asn Leu
98          340          345          350
100 Glu Gln Ala Ala Tyr Ala Arg Asp Ala Leu Ala Lys Ala Val Tyr Ser
101          355          360          365
103 Arg Thr Phe Thr Trp Leu Val Arg Lys Ile Asn Arg Ser Leu Ala Ser
104          370          375          380
106 Lys Asp Ala Glu Ser Pro Ser Trp Arg Ser Thr Thr Val Leu Gly Leu
107 385          390          395          400
109 Leu Asp Ile Tyr Gly Phe Glu Val Phe Gln His Asn Ser Phe Glu Gln
110          405          410          415
112 Phe Cys Ile Asn Tyr Cys Asn Glu Lys Leu Gln Gln Leu Phe Ile Glu
113          420          425          430
115 Leu Thr Leu Lys Ser Glu Gln Glu Glu Tyr Glu Ala Glu Gly Ile Ala
116          435          440          445
118 Trp Glu Pro Val Gln Tyr Phe Asn Asn Lys Ile Ile Cys Asp Leu Val
119          450          455          460
121 Glu Glu Lys Phe Lys Gly Ile Ile Ser Ile Leu Asp Glu Glu Cys Leu
122 465          470          475          480
124 Arg Pro Gly Glu Ala Thr Asp Leu Thr Phe Leu Glu Lys Leu Glu Asp
125          485          490          495
127 Thr Val Lys Pro His Pro His Phe Leu Thr His Lys Leu Ala Asp Gln
128          500          505          510
130 Lys Thr Arg Lys Ser Leu Asp Arg Gly Glu Phe Arg Leu Leu His Tyr
131          515          520          525
133 Ala Gly Glu Val Thr Tyr Ser Val Thr Gly Phe Leu Asp Lys Asn Asn
134          530          535          540
136 Asp Leu Leu Phe Arg Asn Leu Lys Glu Thr Met Cys Ser Ser Met Asn
137 545          550          555          560

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143                               580                               585                               590
145 Val Glu Ile Leu Arg Ser Lys Glu Pro Ala Tyr Ile Arg Cys Ile Lys
146                               595                               600                               605
148 Pro Asn Asp Ala Lys Gln Pro Gly Arg Phe Asp Glu Val Leu Ile Arg
149                               610                               615                               620
151 His Gln Val Lys Tyr Leu Gly Leu Met Glu Asn Leu Arg Val Arg Arg
152 625                               630                               635                               640
154 Ala Gly Phe Ala Tyr Arg Arg Lys Tyr Glu Ala Phe Leu Gln Arg Tyr
155                               645                               650                               655
157 Lys Ser Leu Cys Pro Glu Thr Trp Pro Met Trp Ala Gly Arg Pro Gln
158                               660                               665                               670
160 Asp Gly Val Ala Val Leu Val Arg His Leu Gly Tyr Lys Pro Glu Glu
161                               675                               680                               685
163 Tyr Lys Met Gly Arg Thr Lys Ile Phe Ile Arg Phe Pro Lys Thr Leu
164                               690                               695                               700
166 Phe Ala Thr Glu Asp Ser Leu Glu Val Arg Arg Gln Ser Leu Ala Thr
167 705                               710                               715                               720
169 Lys Ile Gln Ala Ala Trp Arg Gly Phe His Trp Arg Gln Lys Phe Leu
170                               725                               730                               735
172 Arg Val Lys Arg Ser Ala Ile Cys Ile Gln Ser Trp Trp Arg Gly Thr
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178 Arg Arg Leu Ile Arg Gly Phe Ile Leu Arg His Ser Pro Arg Cys Pro
179                               770                               775                               780
181 Glu Asn Ala Phe Phe Leu Asp His Val Arg Ala Ser Phe Leu Leu Asn
182 785                               790                               795                               800
184 Leu Arg Arg Gln Leu Pro Arg Asn Val Leu Asp Thr Ser Trp Pro Thr
185                               805                               810                               815
187 Pro Pro Pro Ala Leu Arg Glu Ala Ser Glu Leu Leu Arg Glu Leu Cys
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190 Met Lys Asn Met Val Trp Lys Tyr Cys Arg Ser Ile Ser Pro Glu Trp
191                               835                               840                               845
193 Lys Gln Gln Leu Gln Gln Lys Ala Val Ala Ser Glu Ile Phe Lys Gly
194                               850                               855                               860
196 Lys Lys Asp Asn Tyr Pro Gln Ser Val Pro Arg Leu Phe Ile Ser Thr
197 865                               870                               875                               880
199 Arg Leu Gly Thr Glu Glu Ile Ser Pro Arg Val Leu Gln Ser Leu Gly
200                               885                               890                               895
202 Ser Glu Pro Ile Gln Tyr Ala Val Pro Val Val Lys Tyr Asp Arg Lys
203                               900                               905                               910
205 Gly Tyr Lys Pro Arg Pro Arg Gln Leu Leu Leu Thr Pro Ser Ala Val
206                               915                               920                               925
208 Val Ile Val Glu Asp Ala Lys Val Lys Gln Arg Ile Asp Tyr Ala Asn
209                               930                               935                               940
211 Leu Thr Gly Ile Ser Val Ser Ser Leu Ser Asp Ser Leu Phe Val Leu

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212 945          950          955          960
214 His Val Gln Arg Glu Asp Asn Lys Gln Lys Gly Asp Val Val Leu Gln
215          965          970          975
217 Ser Asp His Val Ile Glu Thr Leu Thr Lys Thr Ala Leu Ser Ala Asp
218          980          985          990
220 Arg Val Asn Asn Ile Asn Ile Asn Gln Gly Ser Ile Thr Phe Ala Gly
221          995          1000          1005
223 Gly Pro Gly Arg Asp Gly Ile Ile Asp Phe Thr Ser Gly Ser Glu Leu
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258 tgtcctgctg gagaatttca ccagtggagg tgcccttcatt gagaacctcc ggcggcgggt 180
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322 <212> TYPE: PRT

323 <213> ORGANISM: Artificial Sequence

325 <220> FEATURE:

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327 Peptide Overlapping Consensus Start Site

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/893,371

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